OIPE IAP8
DEC 12 2005
PATENT & TRADEMARK OFFICE

```
-60   tgaaaagatagaataaatggcctcgtg

1     ATGGCGCGGCCAGCGCTGCTGGGCGAG
1      M  A  R  P  A  L  L  G  E

61    GGCCAAGTTGCCGCGGCCACAGAAGTT
21     G  Q  V  A  A  A  T  E  V

121   GAAAATCTCTGCACGATAATATGGACG
41     E  N  L  C  T  I  I  W  T

181   ACTCTCAGATATTTTAGTCACTTTGAT
61     T  L  R  Y  F  S  H  F  D

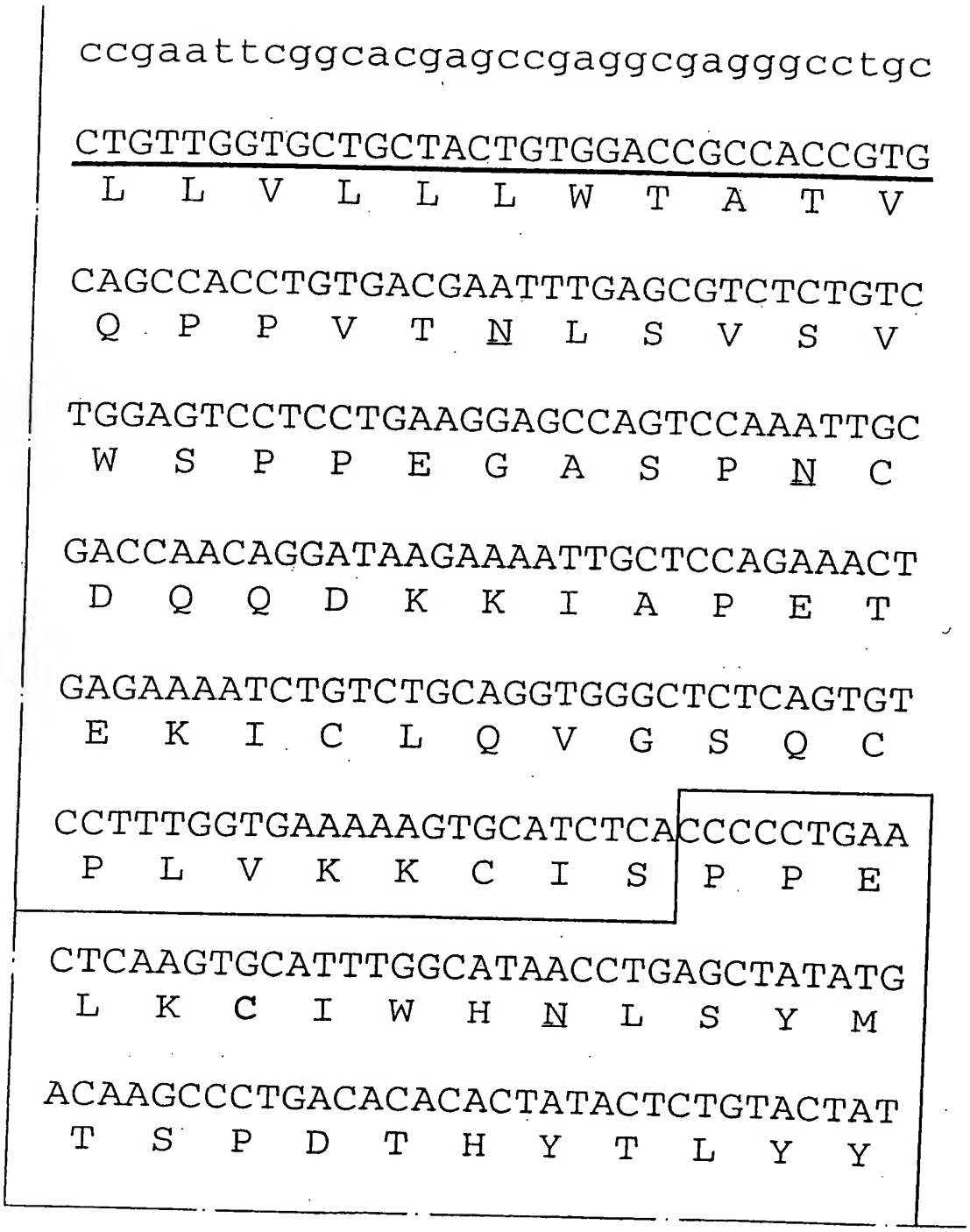
241   CATCGTAAAGAGGAATTACCCCTGGAT
81     H  R  K  E  E  L  P  L  D

301   AGTGCCAATGAAAGTGAGAAGCCTAGC
101    S  A  N  E  S  E  K  P  S

361   GGTGATCCTGAGTCCGCTGTGACTGAG
121    G  D  P  E  S  A  V  T  E

421   AAGTGTTCCTGGCTCCCTGGAAGGAAT
141    K  C  S  W  L  P  G  R  N
```

Fig. 1A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Q P P V T N L S V S V
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P L V K K C I S P P E
CTCAAGTGCATTTGGCATAACCTGAGCTATATG
L K C I W H N L S Y M
ACAAGCCCTGACACACACTATACTCTGTACTAT
T S P D T H Y T L Y Y

Fig. 1B

481	TGGTACAGCAGCCTGGACAAAAGTCGT
161	W Y S S L E K S R
541	ATTGCTTGTTCCTTTAAATTGACTAAA
181	I A **C** S F K L T K
601	ATAATGGTCAAGGATAATGCTGGGAAA
201	I M V K D N A G K
661	TCCTATGTGAAACCTGATCCTCCACAT
221	S Y V K P D P P H
721	TTAGTGCAGTGGAAGAATCCACAAAAT
241	L V Q W K N P Q N
781	GTCAATAATACTCAAACCGACCGACAT
261	V N N T Q T D R H
841	AATTCCGAATCTGATAGAAACATGGAG
281	N S E S D R N M E
901	GCCGACGCTGTCTACACAGTCAGAGTA
301	A D A V Y T V R V
961	AACAAACTGTGGAGTGATTGGAGTGAA
321	N K L **W S D W S** E

Fig. IC

```
CAATGTGAAAACATCTATAGAGAAGGTCAACAC
 Q  C  E  N  I  Y  R  E  G  Q  H

GTGGAACCTAGTTTTGAACATCAGAACGTTCAA
 V  E  P  S  F  E  H  Q  N  V  Q

ATTAGGCCATCCTGCAAAATAGTGTCTTTAACT
 I  R  P  S  C  K  I  V  S  L  T

ATTAAACATCTTCTCCTCAAAAATGGTGCCTTA
 I  K  H  L  L  L  K  N  G  A  L

TTTAGAAGCAGATGCTTAACTTATGAAGTGGAG
 F  R  S  R  C  L  T  Y  E  V  E

AATATTTTAGAGGTTGAAGAGGACAAATGCCAG
 N  I  L  E  V  E  E  D  K  C  Q

GGTACAAGTTGTTTCCAACTCCCTGGTGTTCTT
 G  T  S  C  F  Q  L  P  G  V  L

AGAGTCAAAACAAACAAGTTATGCTTTGATGAC
 R  V  K  T  N  K  L  C  F  D  D

GCACAGAGTATAGGTAAGGAGCAAAACTCCACC
 A  Q  S  I  G  K  E  Q  N  S  T
```

Fig. 1D

```
1021   TTCTACACCACCATGTTACTCACCATT
341     F   Y   T   T   M   L   L   T   I

1081   CTTTTTTTACCTGAAAAGGCTTAAGATC
361     L   F   Y   L   K   R   L   K   I

1141   ATTTTTAAAGAAATGTTTGGAGACCAG
381     I   F   K   E   M   F   G   D   Q

1201   ATCTATGAGAAACAATCCAAAGAAGAA
401     I   Y   E   K   Q   S   K   E   E

1261   AAAGCAGCTCCTTGAtggggagaagtg
421     K A A P *

1321   gatttattgcattctccatttgttatc
1381   cttgaaaaacaggcagctcctaagagc
1441   ccaaacccaaaggagctccttccaaga
1501   ccctaaaagcagatgttttgccaaatc
1561   accatcaattcatctaatcaggaattg
```

Fig. 1E

```
CCAGTCTTTGTCGCAGTGGCAGTCATAATCCTC
 P   V   F   V   A   V   A   V   I   I   L

ATTATATTTCCTCCAATTCCTGATCCTGGCAAG
 I   I   F   P   P   I   P   D   P   G   K

AATGATGATACCCTGCACTGGAAGAAGTATGAC
 N   D   D   T   L   H   W   K   K   Y   D

ACGGATTCTGTAGTGCTGATAGAAAACCTGAAG
 T   D   S   V   V   L   I   E   N   L   K

atttctttcttgccttcaatgtgaccctgtgaa


tgggggacttgttaaatagaaactgaaactact
cacaggtcttgatgtgacttttgcattgaaaac
aaagcaagagttcttctcgttccttgttccaat
cccaaactagaggacaaagacaaggggacaatg
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Fig. IF

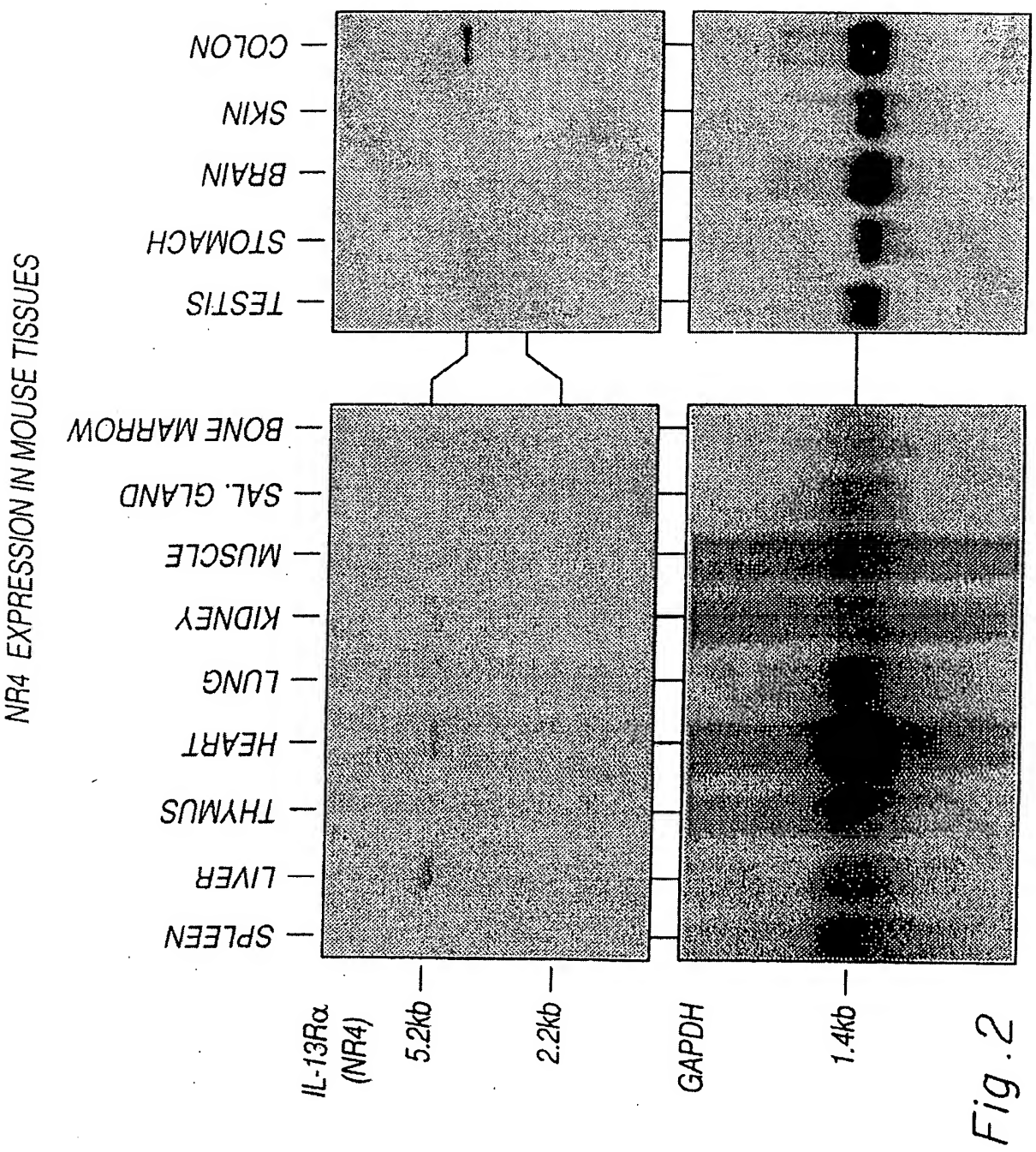

Fig. 2

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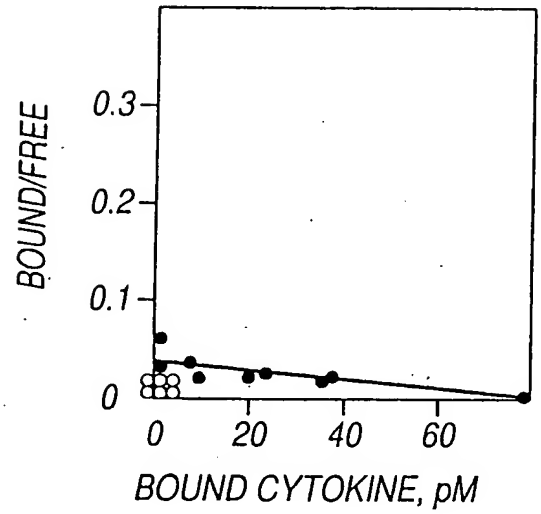


Fig. 3A

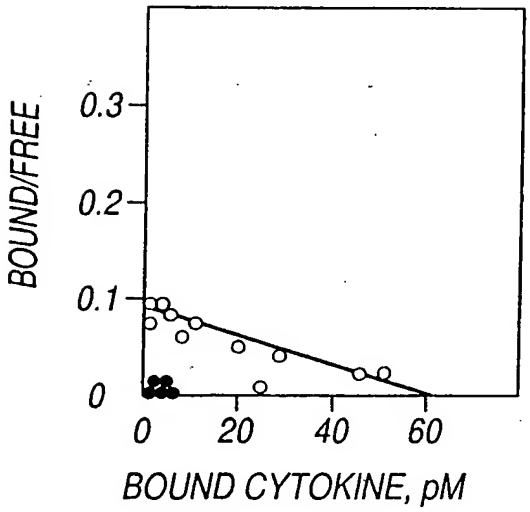


Fig. 3B

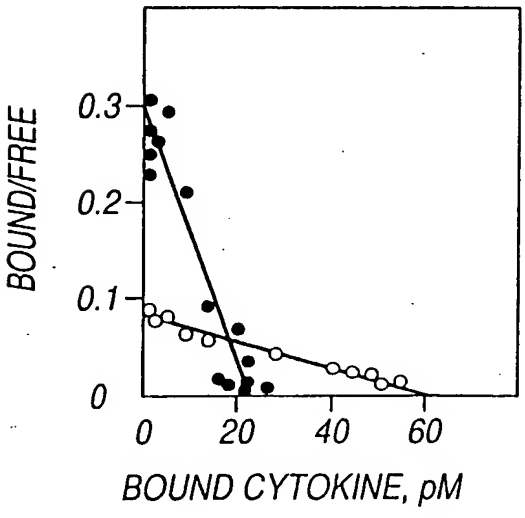


Fig. 3C

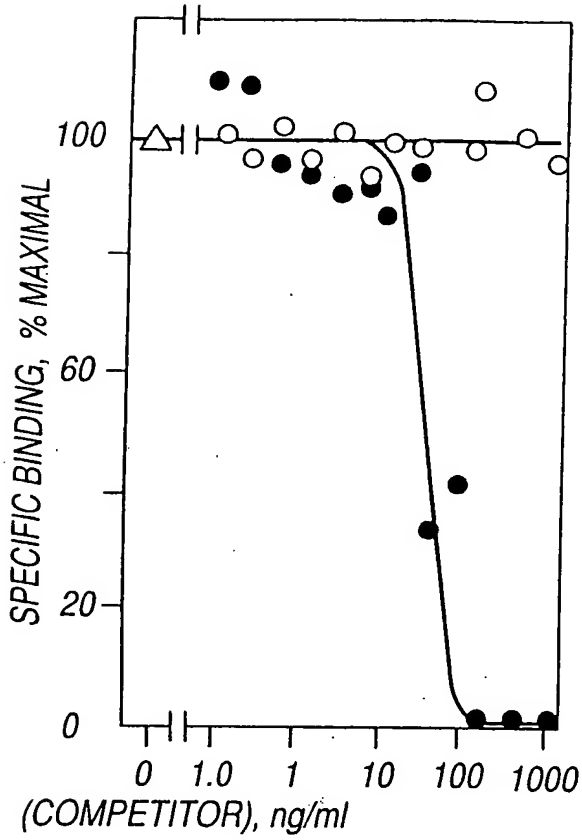


Fig.4A

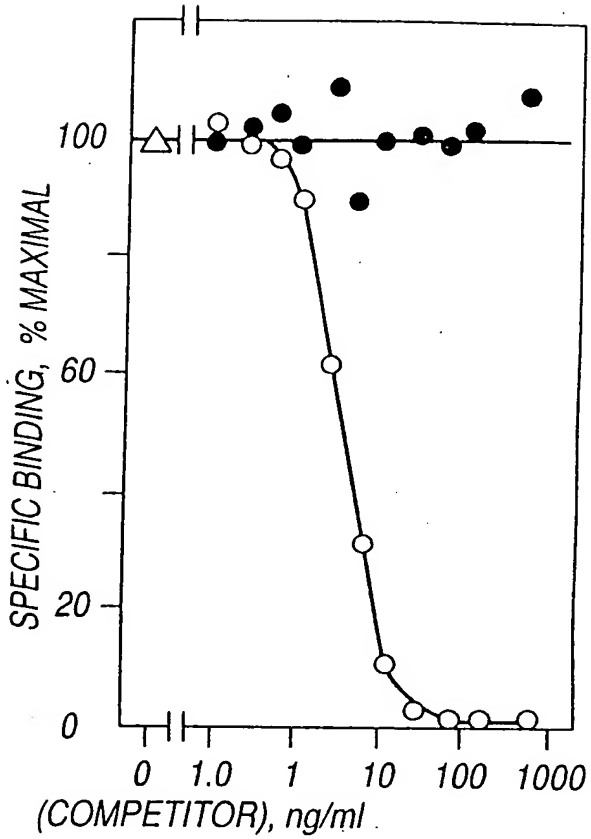


Fig.4B

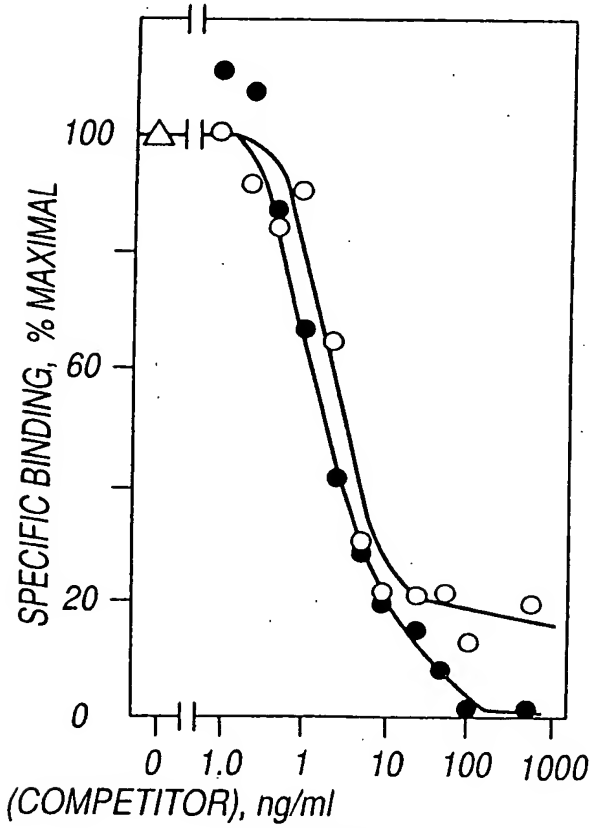


Fig.4C

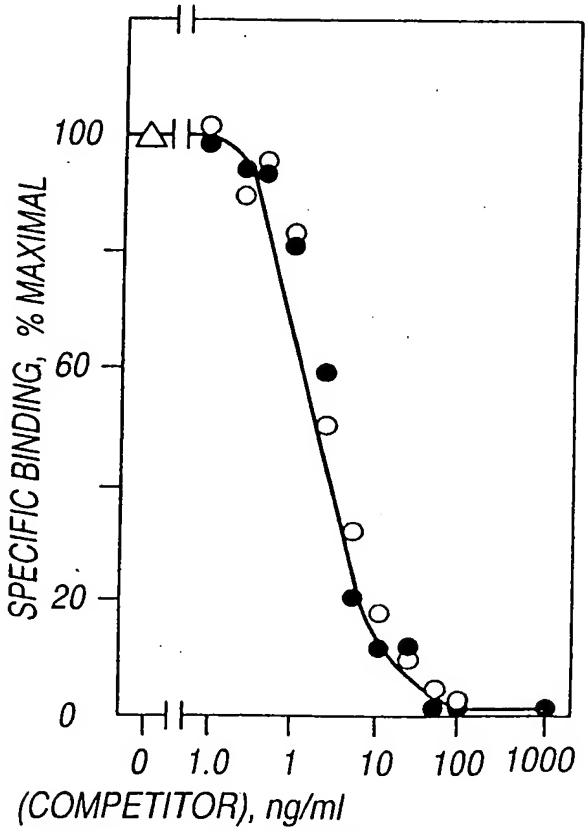
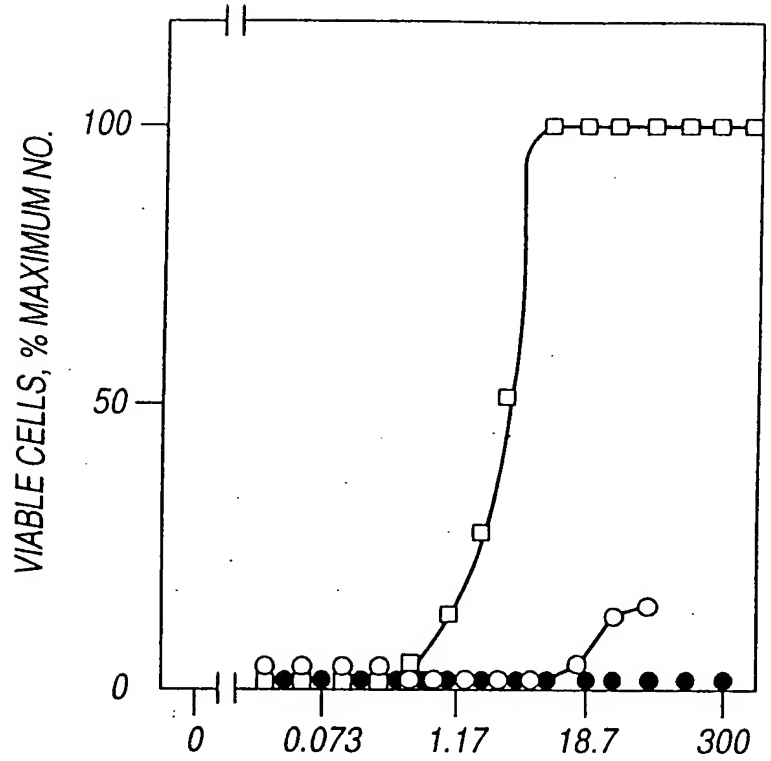


Fig.4D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50
0
VIABLE CELLS, % MAXIMUM NO.
0
0.073
1.17
18.7
300
(CYTOKINE), ng/ml

Fig. 5A

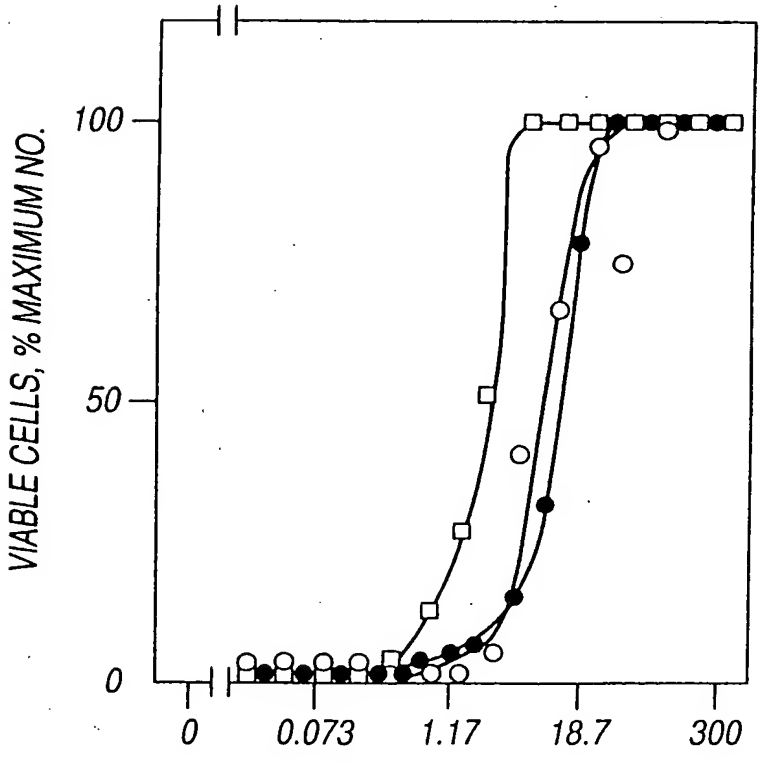
100
50
0
VIABLE CELLS, % MAXIMUM NO.
0
0.073
1.17
18.7
300
(CYTOKINE), ng/ml

Fig. 5B

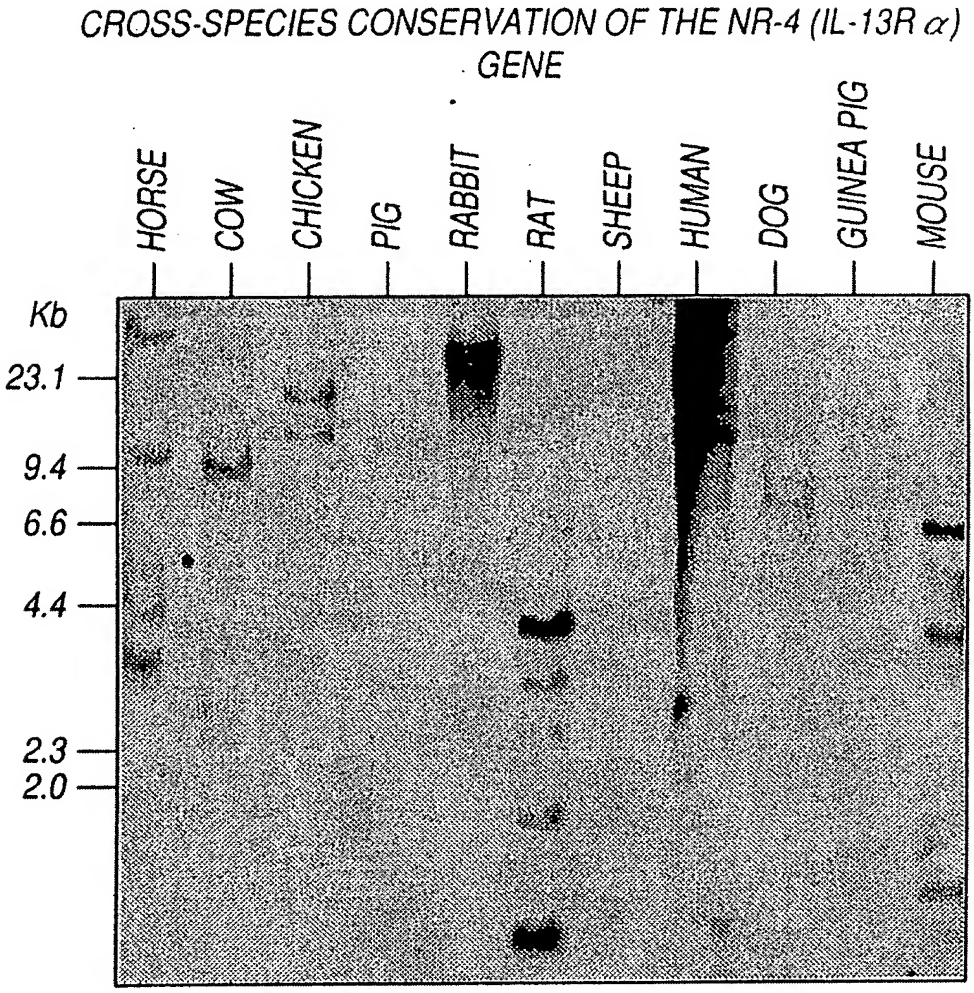

Fig. 6

(major)

DYKDD	DDYKD	DDESR	TEVQP	PVTXL	SV
1	5	10	15	20	25

(minor)

ASISS	SDYKD	DDESR	TEVQP	PVTXL	SV
1	5	10	15	20	25

Fig. 10

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```
H          gagtctaacacggaccaaggagtttaac

M   -60    tgaaaagatagaataaatggcctcgtgc

H            M   E   W   P   A   R   L   C   G
           ATGGAGTGGCCGGCGCGGCTCTGCGGGC
             *           *   *       *
M   1      ATGGCGCGGCCAGCGCTGCTGGGCGAGC
M   1        M   A   R   P   A   L   L   G   E

H            G   G   G   G   A   P   T   E   T
H          GGGGGCGGGGGCGCGCCTACGGAAACTC
             *               *       *   *
M   61     GGCCAAGTTGCCGCGGCCACAGAAGTTC
M   21       G   Q   V   A   A   A   T   E   V

H            E   N   L   C   T   V   I   W   T
H          GAAAACCTCTGCACAGTAATATGGACAT
             *   *   *   *   *       *   *   *
M   121    GAAAATCTCTGCACGATAATATGGACGT
M   41       E   N   L   C   T   I   I   W   T

H            S   L   W   Y   F   S   H   F   G
H          AGTCTATGGTATTTTAGTCATTTTGGCG
               *       *   *   *   *   *
M   181    ACTCTCAGATATTTTAGTCACTTTGATG
M   61       T   L   R   Y   F   S   H   F   D
```

Fig. 7A

```
acgtgcggccgggttccgaggcgagaggctgc
     ....       .......... . ....
cgaattcggcacgagccgaggcgagggcctgc

L  W  A  L  L  L  C  A  G  G  G  G
TGTGGGCGCTGCTGCTCTGCGCCGGCGGCGGGGGC
*        *  *  *
TGTTGGTGCTGCTACTGTGGACCGCCACCGTG---
L  L  V  L  L  L  W  T  A  T  V  -

Q  P  P  V  T  N  L  S  V  S  V
AGCCACCTGTGACAAATTTGAGTGTCTCTGTT
*  *  *  *  *  *  *  *  *  *  *
AGCCACCTGTGACGAATTTGAGCGTCTCTGTC
Q  P  P  V  T  N  L  S  V  S  V

W  N  P  P  E  G  A  S  S  N  C
GGAATCCACCCGAGGGAGCCAGCTCAAATTGT
*     *  *  *  *  *  *     *  *
GGAGTCCTCCTGAAGGAGCCAGTCCAAATTGC
W  S  P  P  E  G  A  S  P  N  C

D  K  Q  D  K  K  I  A  P  E  T
ACAAACAAGATAAGAAAATAGCTCCGGAAACT
*     *  *  *  *  *  *  *  *  *
ACCAACAGGATAAGAAAATTGCTCCAGAAACT
D  Q  Q  D  K  K  I  A  P  E  T
```

Fig. 7B

```
H          R  R  S  I  E  V  P  L  N
H          CGTCGTTCAATAGAAGTACCCCTGAATG
                *        *     *  *
M   241    CATCGTAAAGAGGAATTACCCCTGGATG
M   81       H  R  K  E  E  L  P  L  D

H          S  T  N  E  S  E  K  P  S
H          AGCACCAATGAGAGTGAGAAGCCTAGCA
             *     *  *  *  *  *  *  *
M   301    AGTGCCAATGAAAGTGAGAAGCCTAGCC
M   101      S  A  N  E  S  E  K  P  S

H          G  D  P  E  S  A  V  T  E
H          GGTGATCCTGAGTCTGCTGTGACTGAAC
             *  *  *  *  *  *  *  *  *
M   361    GGTGATCCTGAGTCCGCTGTGACTGAGC
M   121      G  D  P  E  S  A  V  T  E

H          K  C  S  W  L  P  G  R  N
H          AAGTGTTCTTGGCTCCCTGGAAGGAATA
             *  *  *  *  *  *  *  *  *
M   421    AAGTGTTCCTGGCTCCCTGGAAGGAATA
M   141      K  C  S  W  L  P  G  R  N

H          W  H  R  S  L  E  K  I  H
H          TGGCACAGAAGCCTGGAAAAAATTCATC
```

Fig. 7C

```
E   R   I   C   L   Q   V   G   S   Q   C
AGAGGATTTGTCTGCAAGTGGGGTCCCAGTGT
*       *   *   *   *   *   *   *   *   *
AGAAAATCTGTCTGCAGGTGGGCTCTCAGTGT
E   K   I   C   L   Q   V   G   S   Q   C

I   L   V   E   K   C   I   S   P   P   E
TTTTGGTTGAAAAATGCATCTCACCCCCAGAA
    *   *   *   *   *   *   *   *   *   *
CTTTGGTGAAAAAGTGCATCTCACCCCCTGAA
P   L   V   K   K   C   I   S   P   P   E

L   Q   C   I   W   H   N   L   S   Y   M
TTCAATGCATTTGGCACAACCTGAGCTACATG
*       *   *   *   *   *   *   *   *   *
TCAAGTGCATTTGGCATAACCTGAGCTATATG
L   K   C   I   W   H   N   L   S   Y   M

T   S   P   D   T   N   Y   T   L   Y   Y
CCAGTCCCGACACTAACTATACTCTCTACTAT
*   *   *   *   *       *   *   *   *   *
CAAGCCCTGACACACACTATACTCTGTACTAT
T   S   P   D   T   H   Y   T   L   Y   Y

Q   C   E   N   I   F   R   E   G   Q   Y
AATGTGAAAACATCTTTAGAGAAGGCCAATAC
```

Fig. 7D

```
                 *           *   *   *   *
M   481   TGGTACAGCAGCCTGGAGAAAAGTCGTC
M   161    W   Y   S   S   L   E   K   S   R

H          F   G   C   S   F   D   L   T   K
H         TTTGGTTGTTCCTTTGATCTGACCAAAG
                   *   *   *       *   *   *
M   541   ATTGCTTGTTCCTTTAAATTGACTAAAG
M   181    I   A   C   S   F   K   L   T   K

H          Q   I   M   V   K   D   N   A   G
H         CAAATAATGGTCAAGGATAATGCAGGAA
           *   *   *   *   *   *   *   *   *
M   601   CAAATAATGGTCAAGGATAATGCTGGGA
M   201    Q   I   M   V   K   D   N   A   G

H          T   S   R   V   K   P   D   P   P
H         ACTTCCCGTGTGAAACCTGATCCTCCAC
           *   *       *   *   *   *   *   *
M   661   ACTTCCTATGTGAAACCTGATCCTCCAC
M   221    T   S   Y   V   K   P   D   P   P

H          L   Y   V   Q   W   E   N   P   Q
H         CTATATGTGCAATGGGAGAATCCACAGA
           *       *   *   *       *   *   *
M   721   TTATTAGTGCAGTGGAAGAATCCACAAA
M   241    L   L   V   Q   W   K   N   P   Q
```

Fig. 7E

```
*   *   *   *   *       *   *   *   *
AATGTGAAAACATCTATAGAGAAGGTCAACAC
Q   C   E   N   I   Y   R   E   G   Q   H

V   K   D   S   S   F   E   Q   H   S   V
TGAAGGATTCCAGTTTTGAACAACACAGTGTC
*               *   *   *               *
TGGAACCT---AGTTTTGAACATCAGAACG TT
V   E   P   -   S   F   E   H   Q   N   V

K   I   K   P   S   F   N   I   V   P   L
AAATTAAACCATCCTTCAATATAGTGCCTTTA
*   *       *   *           *   *       *
AAATTAGGCCATCCTGCAAAATAGTGTCTTTA
K   I   R   P   S   C   K   I   V   S   L

H   I   K   N   L   S   F   H   N   D   D
ATATTAAAAACCTCTCCTTCCACAATGATGAC
*   *   *       *               *
ATATTAAACATCTTCTCCTCAAAAATGGTGCC
H   I   K   H   L   L   L   K   N   G   A

N   F   I   S   R   C   L   F   Y   E   V
ATTTTATTAGCAGATGCCTATTTTATGAAGTA
*   *       *   *   *   *       *   *   *
ATTTTAGAAGCAGATGCTTAACTTATGAAGTG
N   F   R   S   R   C   L   T   Y   E   V
```

Fig. 7F

```
H          E  V  N  N  S  Q  T  E  T
H          GAAGTCAATAACAGCCAAACTGAGACAC
           *  *  *  *     *  *
M   781    GAGGTCAATAATACTCAAACCGACCGAC
M   261    E  V  N  N  T  Q  T  D  R

H          E  N  P  E  F  E  R  N  V
H          GAGAATCCAGAATTTGAGAGAAATGTGG
              *     *        *  *
M   841    CAGAATTCCGAATCTGATAGAAACATGG
M   281    Q  N  S  E  S  D  R  N  M

H          L  P  D  T  L  N  T  V  R
H          CTTCCTGATACTTTGAACACAGTCAGAA
           *     *           *  *  *
M   901    CTTGCCGACGCTGTCTACACAGTCAGAG
M   301    L  A  D  A  V  Y  T  V  R

H          D  D  K  L  W  S  N  W  S
H          GATGACAAACTCTGGAGTAATTGGAGCC
           *     *  *  *  *     *  *
M   961    GACAACAAACTGTGGAGTGATTGGAGTG
M   321    D  N  K  L  W  S  D  W  S

H          T  L  Y  I  T  M  L  L  I
H          ACACTCTACATAACCATGTTACTCATTG
```

Fig. 7G

```
H   N   V   F   Y   V   Q   E   A   K   C
ATAATGTTTTCTACGTCCAAGAGGCTAAATGT
*   *           *       *       *   *
ATAATATTTTAGAGGTTGAAGAGGACAAATGC
H   N   I   L   E   V   E   E   D   K   C

E   N   T   S   C   F   M   V   P   G   V
AGAATACATCTTGTTTCATGGTCCCTGGTGTT
*       *   *   *   *           *   *   *
AGGGTACAAGTTGTTTCCAACTCCCTGGTGTT
E   G   T   S   C   F   Q   L   P   G   V

I   R   V   K   T   N   K   L   C   Y   E
TAAGAGTCAAAACAAATAAGTTATGCTATGAG
    *   *   *   *   *   *   *   *
TAAGAGTCAAAACAAACAAGTTATGCTTTGAT
V   R   V   K   T   N   K   L   C   F   D

Q   E   M   S   I   G   K   K   R   N   S
AAGAAATGAGTATAGGTAAGAAGCGCAATTCC
            *   *   *   *           *   *
AAGCACAGAGTATAGGTAAGGAGCAAAACTCC
E   A   Q   S   I   G   K   E   Q   N   S

V   P   V   I   V   A   G   A   I   I   V
TTCCAGTCATCGTCGCAGGTGCAATCATAGTA
```

Fig. 7H

```
                 *       *       *   *   *   *
M   1021 ACCTTCTACACCACCATGTTACTCACCA
M   341    T   F   Y   T   T   M   L   L   T

H          L   L   L   Y   L   K   R   L   K
H        CTCCTGCTTTACCTAAAAAGGCTCAAGA
                 *   *       *   *   *   *   *   *
M   1081 CTCCTTTTTTACCTGAAAAGGCTTAAGA
M   361    L   L   F   Y   L   K   R   L   K

H          K   I   F   K   E   M   F   G   D
H        AAGATTTTTAAAGAAATGTTTGGAGACC
                 *   *   *   *   *   *   *   *   *
M   1141 AAGATTTTTAAAGAAATGTTTGGAGACC
M   381    K   I   F   K   E   M   F   G   D

H          D   I   Y   E   K   Q   T   K   E
H        GACATCTATGAGAAGCAAACCAAGGAGG
                 *   *   *   *   *   *       *   *
M   1201 GACATCTATGAGAAACAATCCAAAGAAG
M   401    D   I   Y   E   K   Q   S   K   E

H          K   K   A   S   Q   *
H        AAGAAAGCCTCTCAGTGAtggagataat
                 *   *   *
M   1261 AAGAAAGCAGCTCCTTGAtggggagaag
M   421    K   K   A   A   P   *
```

Fig. 7I

```
    *   *       *   *       *       *
TTCCAGTCTTTGTCGCAGTGGCAGTCATAATC
I   P   V   F   V   A   V   A   V   I   I

I   I   I   F   P   P   I   P   D   P   G
TTATTATATTCCCTCCAATTCCTGATCCTGGC
*   *   *   *   *   *   *   *   *   *   *
TCATTATATTTCCTCCAATTCCTGATCCTGGC
I   I   I   F   P   P   I   P   D   P   G

Q   N   D   D   T   L   H   W   K   K   Y
AGAATGATGATACTCTGCACTGGAAGAAGTAC
*   *   *   *   *   *   *   *   *   *   *
AGAATGATGATACCCTGCACTGGAAGAAGTAT
Q   N   D   D   T   L   H   W   K   K   Y

E   T   D   S   V   V   L   I   E   N   L
AAACCGACTCTGTAGTGCTGATAGAAAACCTG
*   *   *   *   *   *   *   *   *   *   *
AAACGGATTCTGTAGTGCTGATAGAAAACCTG
E   T   D   S   V   V   L   I   E   N   L

ttatttttaccttcactgtgaccttgagaaga

tgatttctttcttgccttcaatgtgaccctgt
```

Fig. 7J

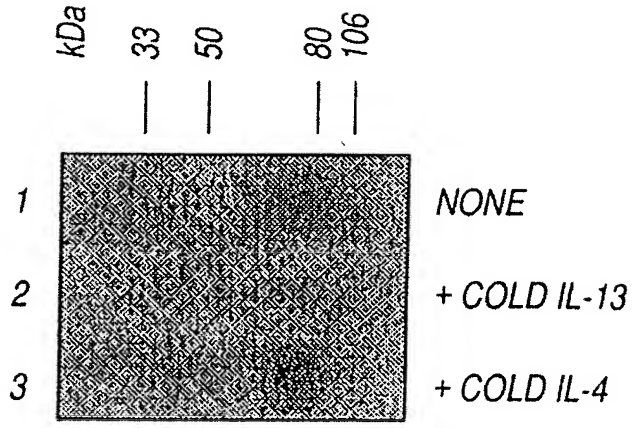

Fig.8

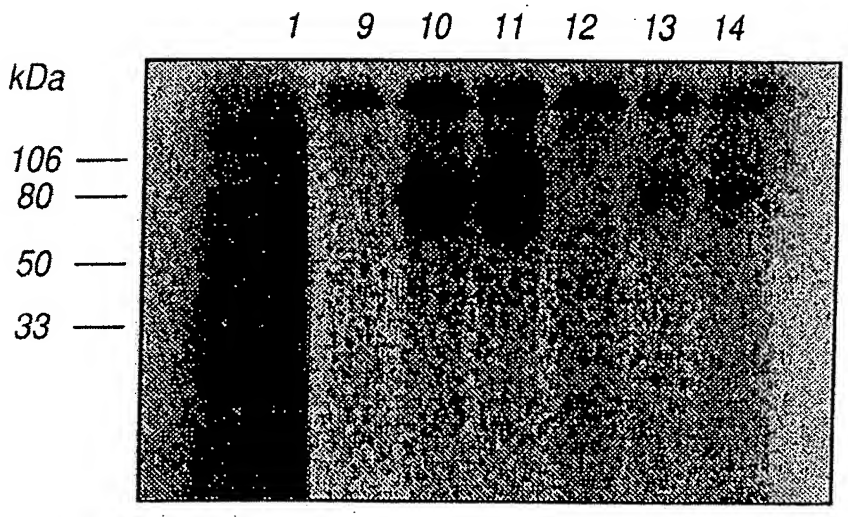

Fig.9

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